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OM protein - nucleic search, using frame\_Plus\_P2n model

Run on: April 5, 2003, 01:50:12 ; Search time 287 Seconds  
(without alignments)  
3452.541 Million cell updates/sec

Title: US-09-847-081B-2

Perfect score: 2270  
Sequence: 1 MSMSTALLWVTPSEVSNG.....IAYAKSLVPPNRTSSPLAKT 440

Scoring table: BiCOSUM62

Xgapop 10.0 Xgapext 0.5  
Ygapop 10.0 Ygapext 0.5  
Fgapop 6.0 Fgapext 7.0  
DelOp 6.0 Delett 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL:frame+P2n.model -DEV=xmlP  
-Q=Cgn2\_1/USP70\_spool/US09847081/runat\_01042003\_120128\_26729/app\_query.fasta\_1..583  
-DB=N\_Geneset\_10102 -QBWT=fastcap -SUFIX=rng -MINMATCH=0.1 -LOOPCL=0  
-LOPEXT=0 -UNITS=bits -STAR=1 -END=1 -MATRIX=blossom62 -TRANS=human40.cdi  
-LIST=45 -DOALIGNN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFILE=pto -NORM=EXT -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09847081@runat\_01042003\_120128\_26729 -NCPU=6 -ICPU=3  
-NO\_XMAP -NO\_NMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=0.5 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N\_Geneset\_101002.\*  
1: /SDS2/gcgdata/geneseq/geneseq/geneseq/geneseq -emb1/NA1980.DAT:/\*  
2: /SDS2/gcgdata/geneseq/geneseq/geneseq/geneseq -emb1/NA1981.DAT:/\*  
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21: /SDS2/gcgdata/geneseq/geneseq/geneseq/geneseq -emb1/NA2000.DAT:/\*  
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23: /SDS2/gcgdata/geneseq/geneseq/geneseq/geneseq -emb1/NA2001B.DAT:/\*  
24: /SDS2/gcgdata/geneseq/geneseq/geneseq/geneseq -emb1/NA2002.DAT:/\*

RESULT 1  
ID AAT166366 standard; cDNA; 1728 BP.  
XX  
AC AAT166366;  
DT 29-JAN-2002 (first entry)

Nicotiana tabacum phytoene synthase coding sequence #1.  
DE Nicotiana tabacum phytoene synthase coding sequence #1.  
XX  
KW Phytoene synthase; zeta carotene desaturase; herbicide; transgenic plant;  
KW plant growth regulator; herbicidal; tobacco; ss.  
XX  
OS Nicotiana tabacum.  
XX  
FH Key  
FT CDS  
FT

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Result No.	Score	Query	Match Length	DB ID	Description
	1	22.0	100.0	1728	24	Nicotiana tabacum phytoene synthase
	2	18.26	80.4	1826	19	Nicotiana tabacum phytoene synthase
	3	18.01	79.3	1712	24	Nicotiana tabacum phytoene synthase
	4	17.99	79.3	1814	19	Nicotiana tabacum phytoene synthase
	5	17.74	78.1	1795	19	Nicotiana tabacum phytoene synthase
	6	17.62	77.6	1316	19	Nicotiana tabacum phytoene synthase
	7	17.51	77.1	1591	17	Malva phytoene synthase
	8	17.44	76.8	1239	19	AV17247
	9	17.37	76.5	1239	21	AAZ91482
	10	17.29	76.2	1646	12	AQ12495
	11	15.95	70.3	2868	19	AV16951
	12	15.57	68.6	1921	19	AV16949
	13	15.42	67.9	1566	21	AAC8162
	14	15.42	67.9	1703	21	AC51520
	15	15.31	67.4	2085	19	AV16948
	16	15.23	67.1	1932	19	AV16950
	17	15.14	66.7	2585	23	AB1600
	18	14.31	63.1	1304	24	ABA91361
	19	13.93	61.4	1397	21	AAZ29145
	20	12.52	55.2	1448	21	AAZ29139
	21	10.78	42.1	1021	21	AAZ29146
	22	10.33	45.5	3485	13	AQ29121
	23	10.33	45.5	992	21	AAZ29144
	24	9.92	43.7	1060	21	AAZ29143
	25	7.81	34.4	888	21	AAZ29140
	26	5.11	22.5	476	21	AAZ29142
	27	4.68	20.6	684	22	AAH44248
	28	4.58	20.2	1509	15	AQ04910
	29	4.42	19.5	749	19	AV03882
	30	4.20	18.5	766	21	AAZ23141
	31	3.78	16.7	56609	21	AAA81459
C	32	3.78	16.7	349980	21	AAF21609
C	33	3.78	16.7	1437668	21	AAA16490
C	34	3.64	16.0	1198	12	AQ13718
C	35	3.64	16.0	1198	17	AT10791
C	36	3.64	16.0	1198	17	AT41743
C	37	3.64	16.0	1198	17	AT10793
C	38	3.64	16.0	1198	18	AT10793
C	39	3.63	16.0	1198	18	AT10793
C	40	3.50	15.4	1232	19	AV19122
C	41	3.50	15.4	1232	20	AAZ2063
C	42	3.50	15.4	1232	24	ABA91354
C	43	3.49	15.4	6918	11	AA005299
C	44	3.47	15.3	1386	13	AQ29122
C	45	3.44	15.2	930	18	AAX23885

## ALIGNMENTS

ALIGNMENTS  
Key Location/Qualifiers  
CDS 247..1556 /\*tag- a

/product- "phytoene synthase"



KW Phytoene synthase; zeta carotene desaturase; herbicide; transgenic plant;  
 KW plant growth regulator; herbicidal; tobacco;  
 XX Nicotiana tabacum.

XX Key CDS  
 FT 333..1565  
 FT /\*tag- a /product- "phytoene synthase"  
 XX DE10022362-A1.  
 PN PF 08-MAY-2000; 2000DE-1022362.  
 PD 15-NOV-2001.  
 XX PR 08-MAY-2000; 2000DE-1022362.  
 XX PA (FARB ) BAYER AG.  
 XX PI Busch M, Hain R;  
 XX WPI; 2002-027336/04.  
 DR P-PSDB; AAM51842.  
 XX PT New nucleic acid encoding tobacco zeta-carotene desaturase, useful for screening compounds with herbicidal activity  
 PT screening compounds with herbicidal activity  
 XX PS Claim 14; Page 21-26; 44pp; German.  
 XX CC The present invention provides the protein and coding sequences of phytoene synthases and zeta-carotene desaturase from Nicotiana tabacum. The sequences can be used to identify compounds capable of altering the expression of these genes, which are therefore useful as plant growth regulators and herbicides. They can also be used to produce transgenic plants. The present sequence is the coding sequence of a tobacco phytoene synthase.  
 XX Sequence 1712 BP; 540 A; 265 C; 421 G; 475 T; 11 other;

## Alignment Scores:

Prod. No :	2.04e-183	Length:	1712	Qy 3 MetSerValAlaLeuLeuIrrpValIserProThrSerGluValIserAsnGlyThrGly 22
Score:	1801.00	Matches:	357	Db 333 ATGCTGTGCTGTATGGTTCTACCT--TGTGAAGTCAAATGGACAGGA 389
Percent Similarity:	87.93%	Conservative:	29	Qy 23 LeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeuAlaArg 42
Best Local Similarity:	81.32%	Mismatches:	24	Db 390 TCTGGATTCAGTCGGAGGAAACGGGTTTGATCTCG-----AGG 437
Query Match:	79.34%	Indels:	29	Qy 43 AspArgAsnLeuMetTrpAsnGlyArgLleLysGlyGlyArgLleLysGly 62
DB:	24	Gaps:	4	Db 438 CATGGAAATTAGTGTGCAATGAGAGAACANAGAGGTGIGAAACAAAGGTGAATT 497
				Qy 63 GlySerLeuLeuAlaAspProArgTyrosSerCysLeuGlyIserArgThrGly 82
				Db 498 GGT-----500
				Qy 83 SerThrPheSerValGlnSerSerLeuAlaLeuSerProAlaGlyGluMet---ThrVal 101
				Db 501 -----TCGTTAAGCTCTGCTATGGCTGGATGGCCAAATGGCACATG 551
				Qy 102 SerSerGluLysLysValTyrraspValValLeuLysGlnAlaAlaLeuValLysArgGln 121
				Db 552 ACATCAGAACAGATGGTTATGATGEGTTAACACGCAGCTTAGTGAAGGCCAG 611
				RESULT 4 AAV03881 ID : AAV03881 standard; cDNA; 1814 BP. XX AC XX DT 29-APR-1998 (first entry)

Phytoene synthase coding sequence from *N. tabacum*.  
 Phytoene synthase; transgenic plant; enhanced carotenoid synthesis;  
 ultra violet absorber; food colour; ss.  
 Nicotiana tabacum

QY	61 AsnPheGlySerLeuIleAlaAspProArgTyrSSerCysLeuGlyGlySerArgGhrGlu	80
XX	AAV03878 standard; cDNA; 1795 BP.	
AC		
XX		
DT	29-APR-1998 (first entry)	
TX	Phytoene synthase coding sequence from N. benthamiana.	
DE		
XX	Phytoene synthase; transgenic plant; enhanced carotenoid synthesis;	
KW	ultra violet absorber; food colour; ss.	
XX	Nicotiana benthamiana.	
OS		
XX		
Key	Location/Qualifiers	
FH	361..1584	
FT		
CD5	/*tag= a	
XX	US5705624-A.	
XX	PD 06-JAN-1998.	
XX	PF 27-DEC-1995; 95US-0579667.	
XX	PR 27-DEC-1995; 95US-0579667.	
XX	(DELL/ ) DELLA-CIOPPA G R.	
PA	(FITE/ ) FITZMAURICE W P.	
PA	(GRILL/ ) GRILL L K.	
PA	(HELM/ ) HELLMANN G M.	
PA	(KUMA/ ) KUMAGAI M H.	
XX	Della-Cioppa GR, Fitzmaurice WP, Grill LK, Hellmann GM;	
PI		
PI	Kumagai MH;	
XX	WPI: 1998-086196/08.	
DR	PR-PSDB, ANW4157.	
XX	DNA encoding tobacco phytoene synthase polypeptides - useful for producing recombinant polypeptides or transgenic plants	
PT		
PT	Claim 1; Column 15-20; 25pp; English.	
XX	This sequence encodes the phytoene synthase from Nicotiana benthamiana. The phytoene synthase coding sequence represents a cDNA of the invention. The isolated nucleic acid molecules are used for producing recombinant polypeptides or transgenic plants with enhanced ability to synthesize carotenoids. Phytoene has been used as a ultra violet absorber and other carotenoids have been used as food colours, animal feeds and in the pharmaceutical and cosmetics industries.	
CC	Sequence 1795 BP; 577 A; 271 C; 434 G; 513 T; 0 other;	
CC	Alignment Scores:	
Pred. No.:	Length: 1795	
Score:	Matches: 351	
	Percent Similarity: 87.07%	
	Best Local Similarity: 79.59%	
Query Match:	Mismatches: 28	
DB:	Indels: 29	
	Gaps: 4	
DB:	1295 ATATTGCTGTTGAAAGGTGGGATAATGGAGAACCTTATGAAAGCAATCCAGAGG 1359	
QY	320 ArgGlyArgValTyrLeuProGlnPheAspGluLeuAAGlnAlaGlyIeuSerAspGluAsp 339	
XX	AlaArgLysPheAspGluSerIleLysGlyValThrGluLeuAspSerIleAspArg 379	
DB:	1235 AGAGGAAGAGTCTACTCAACATGATTAGCTGAGCTGACATGAGTCAGTAGA 1411	
QY	380 TrpProValLeuThrAlaLeuIleIleLeuAspGluIleLeuAspGluIleLeuAsp 399	
DB:	1415 TGGCTGTATGCCCTTCCTTGCTGATGAGCAAGGATACTCGAGCATGAGTCAGTAGA 1474	
QY	400 AspTyrAsnPheThrArgArgAlaValSerLysProLysLeuLeuThrLeu 419	
DB:	1475 GACCAACAACTTCAAGAGCTTAATTCCTTA 1533	



Db 1000 AAGTCTTCATGAGGAAGGTTACAACTGAGCTAGCATGGCCCT 1059  
 Qy 382 ValLeuThrAlaLeuLeuLeuTyArgLysIleLeuAspGluIleGluAlaAspTyr 401  
 Db 1060 GTATGGCACTtCttCTGTGTACCGCCAAATACTCGAGAGTCGAACCAATGACTAC 1119  
 Qy 402 AsnAsnPheThrArgGlyAlaValSerLysProLysLeuLeuThrLeuProfile 421  
 Db 1120 AACAACTTCACAAGAGGTTATGTGACCAAATCAAAARGCTTAATTCCTTACCTAT 1179  
 Qy 422 AlaTyrlAlaLysSerLeuValProProAsnArgThr 433  
 Db 1180 GCTTATGCCAAATCTCTTGCCCCCTAACAAAGAACT 1215

**RESULT 7**

AAQ99323 standard; cDNA; 1591 BP.  
 ID AAQ99323;  
 AC AAQ99323;  
 XX DT 13-APR-1996 (first entry)  
 DE Melon phytene synthase gene.  
 XX KW melon; phytene synthase; ripening; cDNA library; fruit; MEL5;  
 KW antisense; transgenic plant; crop improvement; carotenoid; vector;  
 KW 98.  
 XX OS Cucumis melo.  
 XX PN WO9602650-A2.  
 XX PD 01-FEB-1996.  
 XX PF 06-JUL-1995; 95WO-GB01603.  
 XX PR 22-SEP-1994; 94GB-0010081.  
 PR 18-JUL-1994; 94GB-0010505.  
 XX PA (ZENE ) ZENECA LTD.  
 PI Grierson D, John I, Karvouni Z, Taylor J, Turner A;  
 PI Watson C;  
 XX DR WPI; 1996-105912/11.  
 XX PT New isolated DNA encoding melon phytene synthase - used to  
 PT transform plants to modify carotenoid content and related  
 PT characteristics in plant parts, partic. fruit  
 XX PS Claim 2; Page 15-16; 22Pp; English.  
 CC The sequence encodes melon phytene-synthase (MEL5 gene), and is  
 CC almost full-length. The sequence has been isolated as a cDNA clone  
 CC from a ripening-related cDNA library derived from climacteric melon  
 CC fruit, using the tomato phytene-synthase cDNA (TOM5) as a  
 CC heterologous probe. The MEL5 gene 5'-end has also been isolated by  
 CC polymerase chain reaction and sequenced. The DNA may be used in  
 CC sense or antisense constructs to modify gene expression in plants.  
 CC The carotenoid content and related characteristics of plant parts  
 CC (particularly fruit) may be modified in this way.  
 XX SQ Sequence 1591 BP; 507 A; 237 C; 395 G; 452 T; 0 other;

us-09-847-081B-2 (1-440) x AAQ99323 (1-1591)

Qy 1 MetSerMetSerValAlaLeuLeuLeuTyArgLysIleLeuAspGluIleGluAlaAspTyr 20  
 Db 258 CTCAAGATGCTGTCGCTGTTATGGTTCTCAATGGG 314  
 Qy 21 ThrglyLeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeu 40  
 Db 315 ACAAGTTCTGGAACTGAGTCAGTCGGGGAGAACCTTTTTGATTCATCG----- 365  
 Qy 41 AlaArgAspArgAslLeuMetTrpAsnGlyArg1LeuLysGlyIgIgIArgGlnArgTrp 60  
 Db 366 ---AGGCATAGGAATTGGTGTCCAAATGAGAACTAATGAGGT----- 407  
 Qy 61 AsnPheGlySerLeuLeuAlaAspProArgTyrsSerCysLeuGlyGlySerArgPheGlu 80  
 Db 408 -----GGTGAAGCAACCTAAAT 425  
 Qy 81 LysGlySerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGlyLumetThr 100  
 Db 426 AATGGACGGAATTTCTGACGGCTGCTGCTGATTTGGCTACTCTGAGAACGGGACG 485  
 Qy 101 ValSerSerGluLysLysValtyrAspValLeuLysGlnAlaAlaLeuValIysArg 120  
 Db 486 ATGACATCGAACAGATGCTAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGAGGG 545  
 Qy 121 GluLeuArgSerThrAspAspLeuIysProAspIleValProGlyAsnLeu 140  
 Db 546 CAACTGAGATCTACCAATGAGTTAGAAGTAGGAAAGCCGGATAACCTATTCGGGATTG 605  
 Qy 141 GlyLeuLeuSerGluAlaTyraspArgCysGlyGluIvaIcysAlaGluTyrrAlaLysThr 160  
 Db 606 GGCTGTTGATGTGAGCATATGAGTAATGAGTTAGTGAAGTAGTCAAGAGACG 665  
 Qy 161 PheTyrlLeuglyThrLysIleuMetThrProGluAAArgArgAlaIleTrPAlaIleTy 180  
 Db 666 TTAACTTAACTGAAACTATGCTAAATGACTCCGAGAAAGAGGGCTATCAGGGCATATAAT 725  
 Qy 181 ValTrpCysAIGAIGA9ThrAspGluIvaIAspGlyProAsnAlaSerHisIleThrPro 200  
 Db 726 GTATGGTGCAGAAACAGATGAACTCTGGTGTGATGCCAAACGGCTCATATATCCCCG 785  
 Qy 201 GlnAlaLeuAspArgTrpGluIleGluAspIlePheSerGlyArgProPheAsp 220  
 Db 786 GCACCTGATAGTGGAAATGGTGTGATGCCAAACGGCTCATATATCCCCG 845  
 Qy 221 MetLeuAspAlaAlaLysSerAspThrValSerArgPheProValAspIleGlnProPhe 240  
 Db 846 ATGCTCGATGGTGTGATGCCAAACGGCTCATATATCCCCG 905  
 Qy 241 ArgAspMetIleGluGlyMetArgMetAspLeutPrrSerArgTyrlLysThrAspIle 260  
 Db 906 AGAGATATGATGGAAAGATGGATGCTTACCTTCAGTTGATATTCCGACATT 965  
 Qy 261 GluLeutY-LeutCysTyrtYrValAlaGlyThrValGlyLeuMetSerValProVal 280  
 Db 966 GAACATACCTTATGTTGCTGATGCTTACCTTCAGTTGATATTCCGACATT 1025  
 Qy 281 MetGlyIleAlaProGlnUserLysAlaThrGluSerValYTrasnAlaAlaLeuAla 300  
 Db 1026 ATGGGATATGCCCTGAATCAAAGCAAAACAGAGCTATAATGCTGCTGGCT 1085  
 Qy 301 LeuGlyLeuAlaAspGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgA9 320  
 Db 1086 CTGGGATCGCAATCAATACTAGAGATGTTGAGAAATGCGCAAGAA 1145  

**Alignment Scores:**

Pred. No.:	4.36e-178	Length:	1591
Score:	1751.00	Matches:	344
Percent Similarity:	86.6%	Conservative:	33
Best Local Similarity:	79.08%	Mismatches:	34
Query Match:	77.14%	Indels:	24
DB:	17	Gaps:	3

Qy	361 ArgLysPheAspGluSerGluLysGlyValThrGluLeuAspSerAlaSerArgTRP	380
Db	1266 AGAAAGTCTTTGTGAGCGAGAAAGCGTGCAGAATTGACTCAGCTAGATGAC	1325
Qy	381 ProValLeuThrAlaLeuLeuLeuLeuLeuLeuLeuAspGluIleGluIleAlaAsnASP	400
Db	1326 CCTGTATGGCATTTGGCTCTTACCCAAATACTAGATGAGATGAAGCCATGAC	1385
Qy	401 TyrAsnAsnPheThrArgGalaTyrvValserLysProProLysLeuLeuThrLeuPro	420
Db	1386 TACACAACCTCACAAAGAGAGCATATGGAGCAATAAGAGTTGATGCTACCT	1445
Qy	421 IleLeuTyraAlaLysSerLeuValProProAsnArgThrSerSer	435
Db	1446 ATTGGATATGCCAAATACTCTTGTCCTCTACAAAAACGCCCTCT	1490
RESULT 8		
	AAV17247	8
ID	AAV17247	standard; DNA; 1239 BP.
XX		
AC	AAV17247;	
XX		
DT	28-MAY-1998	(first entry)
XX		
DE	MTOM5,	modified phytoene synthase gene.
XX		
KW	MTOM5; Phytoene synthase; chloroplast targeting sequence; enzyme; tomato	
KW	protein expression enhancement; transgenic plant; carotenoid synthesis;	
KW	lycopene; ds.	
XX		
OS	Lycopersicon esculentum.	
XX		
Key	Location/Qualifiers	
FH	1..1239	
CDS	/*tag= a	"contains an intron"
FT	/*note=	
exon	1..960	
FT	/*tag= b	
FT	/number= 1	
intron	961..990	
FT	/*tag= c	
FT	/number= 1	
FT	991..1236	
exon	/*tag= d	
FT		

present, but produces the same protein on translation. Transgenic plants with enhanced ability to express a selected can be produced by the method. For example, the method can be used to achieve overexpression of a gene specifying an enzyme necessary for carotenoid synthesis in plants (especially phytene synthase), to enhance carotenoid expression, e.g. overexpression of the carotenoid lycopene responsible for the red colouration of developing tomato fruit. Protein expression is enhanced by inserting a gene construct which is altered by maximising the dissimilarity of nucleotide usage whilst maintaining identity of the encoded protein. Known methods of increasing protein production by gene insertion sometimes result in low or no expression (co-suppression), especially when the recombinant and endogenous gene sequences are similar. The method allows enhanced expression whilst avoiding or reducing co-suppression, since sequence similarity between the two genes is sufficiently reduced.

Alignment Scores:		Sequence 1239 BP; 343 A; 24 C; 320 G; 329 T; 0 other;			
Pred. No.:	Score:	Length:			
Percent Similarity:		Matches:		Conservative:	
Best Local Similarity:		343		32	
Query Match:		Mismatches:		34	
DB:		Indels:		24	
Query:		Gaps:		3	
US-09-847-081B-2 (1-440) x AAV17247 (1-1239)					
Qy	3 MetSerValAlaLeuLeutPheValSerProThrSerGluValSerAsnGlyThrGly	Length: 1239		Length: 1239	
Db	1 ATGAGCGTGGCACTRCTTGTGGTGCCCA	Matches: 343		Matches: 343	
Qy	23 LeuLeuAspSerValArgGluGlyAsnArgValPheValSerArgPheLeuAlaArg	Conservative: 32		Conservative: 32	
Db	58 TTATGGAGGTGTAGAGAGGTATAAGATTCTGACAGTC	Mismatches: 34		Mismatches: 34	
Qy	43 AspArgAsnLeuMetTrpAsnGlyArgIleLysLysGlyArgGlnArgTrpAsnPhe	Indels: 24		Indels: 24	
Db	106 CACCGTAACCTTGTTAGTAACGAACTGATAAACGGGGAA	Gaps: 3		Gaps: 3	
Qy	63 GlySerLeuLeuAlaAspProArgTyrosCysLeuGlySerArgThrGluLySGLY	Length: 1239		Length: 1239	
Db	145 -----	Matches: 105		Matches: 105	
Qy	83 SerThrPheSerValGlnSerSerLeuAlaSerProAlaGlyGluMetThrValSer	Conservative: 105		Conservative: 105	
Db	169 AGAAAAGTTCTCAGTTAGATGCAACACCTTGCACACCTTACCGGTGAGAACTATGACT	Mismatches: 168		Mismatches: 168	
Qy	103 SerGluLysValSvalTyrasPvalValLeuLysProAspIleValProGlyAsnIeuglyLeu	Indels: 168		Indels: 168	
Db	229 AGCCGCCAAATGGTTACGAGCTTACGGTAAACCGACATCCAAATACCTGCAAGCTGACTAGTTAACGTCAGTTA	Gaps: 168		Gaps: 168	
Qy	123 ArgSerThrAspAspIleGluValIlysProAspIleValProGlyAsnIeuglyLeu	Length: 1239		Length: 1239	
Db	289 CGTAGTACAACGAACTTGGGTTACGGTAAACCGACATCCAAATACCTGCAAGCTGACTAGTTAACGTCAGTTA	Matches: 1239		Matches: 1239	
Qy	143 LeuSerGluAlaTyrasPargCysGlyGluValCysAlaGluTyralAlaLysThrPhethyR	Conservative: 162		Conservative: 162	
Db	349 CTTCTGAGCTTACGACAGATGCCGAGAGCTTGGCAGATAACCGCTAAACCTTCAAT	Mismatches: 408		Mismatches: 408	
Qy	163 LeuGlyIthrLysLeuMetThrProGluargArgAlaIleTrpAlaIleTrpValIrrp	Indels: 408		Indels: 408	
Db	409 TTGGTACCATGTTGATGACCAATATGGCTTATACGGTATTACGTTGG	Gaps: 408		Gaps: 408	
Qy	203 LeuSpargTrpGluIthrArgLeuGluAspIlePheSerGlyArgProPheAspMetLeu	Length: 1239		Length: 1239	
Db	529 CTTGACAGATGGGAAACCGCTTGGAGGAGTGTAAACGCCGCTAGTACATAACACCCGCTGCT	Matches: 528		Matches: 528	
Qy	223 AspAlaAlaLeuSerAspThrValSerArgPheProyalAspIleGinProhefArgAsp	Conservative: 588		Conservative: 588	

Db 589 GACGGAGGCCATTGTGACACTGTGAGCAATTCCTGTGACATCCAACTTTCGGAC 648  
 QY 243 MetIleGluGlyMetArgMetAspLeuTrpIleSerArgTyrrLysThrPheAspGluLeu 262  
 Db 649 ATGATCGAGGGCATGAGATGGATCCTCTGGTAAGTCCTATAAGAATTGTGACTTG 708  
 QY 263 TyrLeuTrpCystTyrrValAlaGlyThrValGlyLeuMetSerValProValMetGly 282  
 Db 709 TATTTGATCTGCATGCACTGGAGAACGCGGGCTATGTCAGNCATAGCATAGTT 768  
 QY 283 IleLeuProGluSerLysAlaLahThrLysSerItyrAsnAlaLeuAlaLeuGly 302  
 Db 769 ATTGCAACRGAGAGTAAGCTACTACIGATCTGTTAACCCGAGCATAGCATAGTT 828  
 QY 303 LeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArgGlyArg 322  
 Db 829 ATAGCTAACAGCTACAAATACTGAGCTGGATGAGCTGGTAGGGGTGCGT 888  
 QY 323 ValTyrlLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePhala 342  
 Db 889 GTGPAATCCTCCAGGAGCAGTCGCTGAAGCTGGATGAGCTGGTAGGGGTGCGT 948  
 QY 343 GlyArgValThrAspLysTrpArgAsnPheMetLysSglLleGlnArgAlaArgLys 362  
 Db 949 GGTGCTGTTACAGACAAGTGGAGGATTTCACTGAAAGCAGATTCAACCGTGTGAA 1008  
 QY 363 PheAspAspGluSerGluLysGlyVairThrGluLeuAspSerIleSerArgTrpProVal 382  
 Db 1009 TTTCITCGAGCAAGCTGAAAGGGAGTTACTGACTTCATAGTCATAGGTTCCAGT 1068  
 QY 383 LeuThrAlaLeuLeuLeuTyrrArgLysIleLeuAspGluIleGluAlaAsnAspTyAsn 402  
 Db 1069 TGGCCGAGCTGGCTGCTAGATGAGTTGGACGAATCAGGTTAACTATAAT 1128  
 QY 403 AsnPheThrArgArgAlaTyrrValSerIysProLysLeuLeuThrLeuProIleAla 422  
 Db 11129 AATTTTACAAACCTGTTACGTTCTGAGGCAAACATCTATGCTCTTCAATGCT 1188  
 QY 423 TyrLalLysSerIleUvaIProAsnArgThrSerSer 435  
 Db 11189 TACCGTTAACAGCTGGTTCACCAACATPAAAGCACGCTAGC 1227

RESULT 9  
 AAZ99482  
 ID AAZ99482 standard; CDNA; 1239 BP.  
 XX  
 AC AAZ99482;  
 XX  
 DT 03-JUL-2000 (first entry)  
 XX  
 DE cDNA encoding a phytoene synthase polypeptide.  
 XX  
 KW Gibberellic acid; copalydiphosphate synthase; 3beta-hydroxylase;  
 KW 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase;  
 KW seed germination; seedling growth; gibberellin biosynthetic pathway;  
 KW transgenic plant; hypocotyl; epicotyl; ss.  
 XX  
 OS Lycopersicon esculentum.  
 XX  
 FH Key  
 CDS Location/Qualifiers  
 1..1239 /\*tag= a  
 /product= "phytoene synthase"  
 /trans\_except= "(Pos: 1027..1029, aa: Lys)  
 /trans\_except= "(Pos: 1057..1059, aa: Arg)"  
 WO2000009722-A2.  
 XX  
 PD 24-FEB-2000.  
 XX  
 PF 10-AUG-1999; 99NO-US18066.

PR 10-AUG-1998; 98US-0096111.  
 PR 07-JUN-1999; 99US-0137977.  
 XX  
 PA (MONS ) MONSANTO CO.  
 XX  
 PI Brown SM, Elich TD, Heck GR,  
 PI Piller KJ, Rao S, Ream JE;  
 XX  
 DR WPI: 200022351/19.  
 XX  
 PT Obtaining transgenic plant useful for controlling seed germination and  
 PT seedling growth comprising transgene comprising a sequence expressing  
 PT altered levels of an essential hormone  
 XX  
 PS Claim 45; Page 254 -255; 267PP; English.  
 XX  
 CC The present sequence encodes a phytoene synthase polypeptide, which  
 CC is used in the method of the invention. The specification describes  
 CC methods for the inhibition and control of gibberellin acid levels.  
 CC Gibberellic acid levels may be inhibited or controlled by use of  
 CC a chimeric expression construct expressing a RNA or protein which  
 CC suppresses the gibberellin biosynthetic pathway sequence, diverts  
 CC substrate from the pathway, or degrades pathway substrates or products.  
 CC The methods uses copalydilipophosphate synthase, 3beta-hydroxylase,  
 CC 2-oxidase, phytoene synthase, C-20 oxidase, and a 2beta,3beta-hydroxylase  
 CC polynucleotides to achieve this. The method is used to control seed  
 CC germination and seedling growth especially to regulate gene products of  
 CC gibberellin biosynthetic pathway and restoration of normal seed  
 CC germination, in transgenic plants. The plants produced are gibberellin  
 CC deficient, and have shortened hypocotyl and/or epicotyl phenotypes  
 CC compared to normal plants.  
 XX  
 SQ Sequence 1239 BP; 376 A; 208 C; 316 G; 339 T; 0 other;

Alignment Scores:  
 Pred. No.: 9.71e-177 Length: 1239  
 Score: 1737.00 Matches: 342  
 Percent Similarity: 86.374 Mismatches: 32  
 Best Local Similarity: 78.988 Indels: 35  
 Query Match: 76.528 DB: 21  
 DB: 21 Gaps: 3

US-09-847-081B-2 (1-440) x AAZ99482 .(1-1239)  
 Qy 3 MetSerValAlaLeuLeuTrpValSerProThrSerGluValSerAsnGlyThrGly 22  
 Db 1 ATGTCGTGCTGCTGTTATGGTGTCTCCATGGCAAAAGT 57

Qy 23 LeuLeuAspSerIleArgGluGlyAsnArgValPheValSerSerArgPheLeuAlaArg 42  
 Db 58 TTTATGGAAATCAGTCGGGAGGAAACCTTTTGATTTCATGG-----AGG 105  
 Qy 43 ASPArgAsnLeuMetTrpAsnGlyArgLysLysGlyGlyArgGlnArgTrpAsnPhe 62  
 Db 106 CATAGAAATTGGGTTCGAATGAGAAATAGAGGT----- 144

Qy 63 GlySerLeuLeuAlaAspProArgTyrSerCysLeuGlyGlySerArgThrGlyLysGly 82  
 Db 145 -----GGTGGAAAGCAGAAACTTAATATGGAA 168

Qy 83 SerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMetThrValSer 102  
 Db 169 CGGAAATTTCTGAGGGCTACTCCATCTGAGAAACGACCATGACA 228

Qy 103 SerGluLysLysValTyrrAspValLeuLysGlnAlaAlaLeuValLysArgGlnLeu 122  
 Db 229 TCGCAACAGATGGCTCATGATGTTGAGAGGGAACTGAGGCAACTG 348

Qy 123 ArgSerThrAspAspLeuLysLysProAspLysLeuValValProGlyAsnLeuLeu 142  
 Db 289 AGTCTTACCAATGTTAGAAGTGAAGCTGGGATATACCTATCCGGGAATTGGCTTG 348

Qy	143	LeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGluTyrAlaLysThrPheTyr 162
Db	349	TGAGTGAAGCTATGATAGGTGGTGAAGTATGGCAAGTAGTGGCAANGCTTTAAC 408
Qy	163	LeuGlyThrLysLeuIleThrProGluArgArgArgAlaIleTrpAlaLysTyrValTrp 182
Db	409	TGAGACTATGCTATGACTCCGGAGAGAAGGGTATCTGGCAATAATATATGG 468
Qy	183	CysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleIleProGlnAla 202
Db	469	TGAGAAACAGATGAACTGTTGACTGTGATGCCCAAAAGCATACTATAATTACCCGGCAGGCC 528
Qy	203	LeuAspArgGlyPheGluAspIlePheSerGlyArgProPheAspMetLeu 222
Db	529	CTAGGATGGGAAATAAGCTAGAGAGTTTCATAGGGGCCATTGACATGCTC 588
Qy	223	AspAlaAlaLeuSerAspPheTyrValSerArgPheProValAspIleGlnProPheArgAsp 242
Db	589	GATGGCTCTTGTGCGCATACAGTTCAACTTCAAGTTGATATTCAGCCATTGAGAGAT 648
Qy	243	MetIleGluGlyMetArgMetAspLeuIleTrpIleSerArgGlyTyrLysThrPheAspGluLeu 262
Db	649	ATGATTCGAGGAATGCGTGGCTATGGACTTGAGAAAATCGAGATCACAAAACACTCGACAACTA 708
Qy	263	TyrLeuIrrCysteTyrrTyrrValAlaGlyThrValGlyLeuMetSerValProValMetGly 282
Db	709	TACCTTATTTGTTATGTTATGTTGCTGGTACGTTGGTTGAGTTGAGGGT 768
Qy	283	IleAlaProGluSerIlysAlaIthrThrGluSerValTyrasnAlaIaleAlaIeuGly 302
Db	769	AATGCCCTGATCAAGGCACACAAGAGCCGATATAATGCGCTTGGCTGGGG 828
Qy	303	IeuAlaLysGlnIleThrAsnIleLeuArgAspPheValGlyGluAspAlaArgGlyArg 322
Db	829	ATTCGCAATCTTCAATTTCTAACATCTCAGAGATGTTGGAGAGATGCCAGAAAGAAAGA 888
Qy	323	ValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspIlePheAla 342
Db	889	GTCATCTGGCTCAAGTGAATTAAGCAGATGTTGGAGAGATGCCAGAAAGAAAGA 948
Qy	343	GlyArgValThrAspIlysPheAspIlysPheAsnPhenKetLyAsylsGlnIleGlnArgAlaArgLys 362
Db	949	GGAGGTGACCGATAATGGAACTTATGAAAGAAACAATATAGGGCAAGAAAG 1008
Qy	363	PhePheAspGluSerGluLysGlyValThrGluLeuAspSerAlaSerArgTrpProVal 382
Db	1009	TTCTTGTAGGCGAGAAATGCCGAGACAAATGAGCTCAGCTAGTATTCCCTGTAA 10656
Qy	383	LeuThrAlaLeuIleLeuIleTyrArgLysIleLeuAspGluIleGluAlaAsnAspTyrAsn 402
Db	1069	TGGCATCTTGGCTGCTGTAACGGAAAATAATAGTAGAGATTGAAACCAATGACAAC 1126
Qy	403	AsnPheThrArgArgAlaTyrValSerLysProLysSleLeuThrIleProIleAla 422
Db	1129	AATCTCAAAACAGAGCTATGAGAAATCAAAAGTGTAGTCATTACCTATTGCA 1188
Qy	423	TyrTyrAlaLysSerLeuValProProAsnArgThrSerSer 435
Db	1189	TATGCAAATCTCTGNCCTACACAAAAGTGTAGTCATTACCTATTGCA 1227
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XX	XX	18-SEP-1991 (first entry)
DE	XX	Tomato fruit ripening related gene pTOM5.
XX	XX	ripening; lycopene; transgenic tomato; 35.
KW	XX	Lycopersicon esculentum var. Alisa Craig.
OS	XX	





Db	922	ATATGCTATGGTGTAGGACAGATGAGCTAACGGTCARACATA	981
Qy	199	ThrProGlnAlaLeuAspArgTgIplglutheArgLeuGluAspIlepheSerGlyArgPro	218
Db	982	AATCCGCGTTAGATAGTGAAAGCAGATGAGATGCTTCAAGGGCACCT	1041
Qy	219	PheAspMetLeuAspAlaLeuSerAspHrValserArgPheProValAspIleGin	238
Db	1042	TITGATATGCTGTTACCTGATGCCATTACCAAGTATCTGACTTCAG	1101
Qy	239	ProPheArgAspMetIleGluGlyMetArgMetAspIleTrplysSerArgTyrIleThr	258
Db	1102	CCATTTAGATGATGAGATGAGATGCGATGGCTCTGAGAAATCAGATAACAGAAT	1161
Qy	259	PheAspGluLeutYleIeuTyrCysPtyrTyrylvalAlaGlyIthrValGlyIeumMetSerVal	278
Db	1162	TTTCGATGAGCTGTATTTTACTGCTTATGGCTGTCAGTGGCTGTATGGTGTGA	1221
Qy	279	ProValMetGlyIleAlaProGluSerLysAlaIleThrGluSerValTyrAsnAlaAla	298
Db	1222	CCAGTATGGCATTCGACCTGAACTTAAGGCCAACACAGAACAAAGTGTGATAATCAGCT	1281
Qy	299	LeuAlaLeuGlyLeuAlaAsnGlnIleuthrAsnIleLeuArgAspValGlyGluAspAla	318
Db	1282	TTATCTTGGGATTCGAAACCCTGACTAACATCTAGGGATGTTGGAGAACATGCCA	1341
Qy	319	ArgArgGlyArgValtryLeuProGlnAspGluIleAlaGlnIaglyIeueSerAspGlu	338
Db	1342	AGAAAGGGAAAGTGTGACCTACCTCTGAGCTAACATGGCTGGTATCAGATGAG	1401
Qy	339	AspIlePheAlaGlyArgValthrAspIleTrpArgAsnIhemetylLysGlnIleGln	358
Db	1402	GACATTTTGTGGAAAAGTACAGACAAATGGAGATTTTATAAGGCAAACTCAA	1461
Qy	359	ArgGlyArgLysPheIleAspGluSerGluLysGlyValThrGluIleAspSerAlaSer	378
Db	1462	AGGGCTGAAATTCATGATGATGAGAAAAAGCTCCCGGACTCTACCTCCCGAGC	1521
Qy	379	ArgTrpProValLeuThrAlaLeuIleLeuIleLeuAspGluIleGluIala	398
Db	1522	ATGATGCTGTGTTGGCCAGCTTGTGTTTATAGAAAATATUGATGGATGAAAGCA	1581
Qy	399	AsnAspTyrAsnAsnPheThrArgAlaItyValserIbysProLysLeuLeuThr	418
Db	1582	AATGACTACACAATTCACAAAAGGGCTTATGTTAACAGGCAGAAAGCTATTAGCT	1641
Qy	419	LeuProIleAlaItyValAlaIysSerIeu	427
Db	1642	ATGCCCTGAGATGGCCAAGTCTCTC	1668
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XX	XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 56485.	
DE	DE	Hybridisation assay; genetic mapping; gene expression control;	
KW	KW	protein identification; signal transduction pathway;	
KW	KW	metabolic pathway; promoter; termination sequence; ss.	
XX	XX	Arabidopsis thaliana.	
OS	XX		
EP1033-05-A2.	XX		
PN	XX		
DP	DP	18-OCT-2000 (first entry)	
PD	PD		
PP	PP	25-FEB-2000; 2000EP-0301439.	

PR 13-JUL-1999; 99US-0143542.  
 PR 14-JUL-1999; 99US-0143624.  
 PR 15-JUL-1999; 99US-0144005.  
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PR 04-OCT-1999; 99US-0157117.  
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 PR 18-OCT-1999; 99US-0159384.  
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 PR 26-OCT-1999; 99US-0161361.  
 PR 28-OCT-1999; 99US-0161920.  
 PR 28-OCT-1999; 99US-0161921.  
 PR 28-OCT-1999; 99US-0161922.  
 PR 29-OCT-1999; 99US-0162142..

## Alignment Scores:

Pred. No.: 1.25e-155  
 Score: 1542.00  
 Percent Similarity: 81.86%  
 Best Local Similarity: 72.11%  
 Query Match: 67.93%  
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 QY 153 ATGTTCTTCCTGTTAGCAGTGTATTGGGTCTACTTCCTCTPAATCCAGACCAATG 212  
 QY 19 AsnGlyThrGlyLeuLeuAspSerValArgGluGlyAsnArgValPheValSerArg 38  
 DB: 213 AACAAATTGGGTTGGTTA-----AGGGTTCTAGATCTCTAGA 251  
 QY 39 PhelLeuAlaArgAspGlySerLeuIleAlaAspProArgTyr-SerCysLenglyGlySerAr 78  
 DB: 252 CTGTTCTTCCTGTTAGCAGTGTATTGGGTCTACTTCCTCTPAATCCAGACCAATG 252  
 QY 58 nArgTrpAsnPheGlySerGluLysValtyraspValLeuIleGlySerAr 78  
 DB: 300 CAGATCCACACTTGAGTCTTCCT-----TTGTAAGGGACCGGA 338  
 QY 78 gThsGluLysGlySerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyG 98  
 DB: 339 AGTAGAGAATT-GGTGTT-----GTGCTCTCAAGCTTAGTAGGAAAGTCCTCTGGAGA 391  
 QY 98 uMetThrValSerGluLysValtyraspValLeuIleGlySerAr 78  
 DB: 392 GATAGCTCTTCATGTGAGGAAAGTTACAATGCTGCTGTTGACAAGCTGCTTGGT 451  
 QY 118 LysArgGlnLeuArgSerThrAsp---AspLeuGluVallys-----ProAspIleva 135  
 DB: 452 GAACAAACGCTAACGCTAACGCTCTCTATGACCTCTGTCAGAAGTGTGTGT 511

Qy	135	IvalProGlyAsnLeuGlyLeuLeuSerGluAlaTyrAspArgCysGlyGluValCysAl	155	
Db	512	TCCTCCCGAGCTTGCTTGTGGTTGAGCTTATGATGCTTGTGAGGTTCGCG	571	
Qy	155	AGIUTYRALYSTHRPHETYLLEUGLYTHRLYSLEUMETTYPRLGARGARGARGA	175	
Db	572	TGATATGCTAACGTTTAACCTGAACTTGCTATGAGACCCGAAGCGAAAGGC	631	
Qy	175	AIETTPDALLTYRVALTYRVALTYRCYSARGAARGHRAASPGI	195	
Db	632	GATTGGCCAACTACGTTGCTGAGACTGATGAACTGATGAACTGATGAA	691	
Qy	195	ASERHISILETHPRGQLNLALEWASPGI	215	
Db	692	TTCACATATAACTCCCCATGCCATTAGCTTAGTAGTAAAGCAGCTTTCG	751	
Qy	215	rGlyArgProPheAspMetLeuAspAlaAlaLeuSerAspThrValSerArgPheProva	235	
Db	752	TGGTGCCTCTTCGATATGCTGATGCTGATGCTGATGCTGATACAGTGTAGATA	811	
Qy	235	LASPLLeGlnProPheArgAspMetIleGluGlyMetArgMetAspLeutPlysSerAl	255	
Db	812	CGATATTAGCCATTTCGACATGAACTGAAATCGAG	871	
Qy	255	gTylLysrPhAspGluLeutYrLeutYrCystYtyrValAlagLysValgLe	275	
Db	872	ATACAGAACACTGATGATGATGATGATGATGATGATGATGATGATGATGATG	931	
Qy	275	WMTSERVAlProValMetGlyLeiAlaProGluUserLysAlaThrThrGluSerValty	295	
Db	932	GATGGCGTTCGGTTATGGGAACTCGATCTAAGTCGAAGAACACCGAAAGTTA	991	
Qy	295	RASDAlaAlaLeuAlaGlyLeuAlaAsnGlnLeutHAsnIleLeuArgAspValG	315	
Db	992	CAAGGCTGGCTTGCCCTGGATTAGCCATTACTAGCATACATCGAGCTTGG	1051	
Qy	315	yGluAspAlaArgArgGlyArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGly	335	
Db	1052	CGARAGATGGAGAGACATATGCCGAAAGGTACTGATAATGGAAACTCTATGAAAT	1171	
Qy	335	userAspGluAspIlePhaAlaGlyArgAlaThrasPlyStPArgAsnPhmethylsly	355	
Db	1112	TTCAAGATGGAGACATATGCCGAAAGGTACTGATAATGGAAACTCTATGAAAT	1171	
Qy	355	sGlnIleGlnArgAlaArgLysPheAspGluSerGluLysGlyVallThrGluLeuAs	375	
Db	1172	GCAGCTTAACGAGCAAGATGTCCTGACGAGCTGAAAGGGCTACGGAGCAG	1231	
Qy	375	pSerAlaSerArgTrpProValLeuIleLeuTyrArgLysIleLeuAspG	395	
Db	1232	TGCCGCTACAGTGGCTGATGGCTCATGCTATGCTAGAGGAAATCTGGAGCA	1291	
Qy	395	uIleGluAlaAspTyrAspTyrAspTyrAspTyrAspTyrAspTyrAspTyrAspTyr	415	
Db	1292	GATGAAAGGAAATGATTACACAACTTACTAAGAGCTTATGTGGGAAGTCANGAA	1351	
Qy	415	sLeuLeutYrLeuProIleAlaTyrAlaLysSerLeuValProProAsnArgThrSerSe	435	
Db	1352	AATGGCAGTTGCCATTGCTATGCTTAATCAGTACTA-----AACTCTAAC	1402	
Qy	435	r 435		
Db	1403	T 1403		
RESULT	14			
ID	AAC35120	standard; DNA; 1703 BP.		
XX				
AC				
XX				
DT	17-OCT-2000	(first entry)		
XX				
DE		Arabidopsis thaliana DNA fragment SEQ ID NO : 9067.		
PR				

23-JUN-1999; 99US-0140353.  
 PR 23-JUN-1999; 99US-0140354.  
 PR 24-JUN-1999; 99US-0140695.  
 PR 28-JUN-1999; 99US-0140823.  
 PR 29-JUN-1999; 99US-0140991.  
 PR 30-JUN-1999; 99US-0141287.  
 PR 01-JUL-1999; 99US-0141842.  
 PR 01-JUL-1999; 99US-0142154.  
 PR 02-JUL-1999; 99US-0142055.  
 PR 06-JUL-1999; 99US-0142390.  
 PR 08-JUL-1999; 99US-0142803.  
 PR 09-JUL-1999; 99US-0142920.  
 PR 12-JUL-1999; 99US-0142977.  
 PR 13-JUL-1999; 99US-0143255.  
 PR 14-JUL-1999; 99US-0143542.  
 PR 15-JUL-1999; 99US-0143624.  
 PR 16-JUL-1999; 99US-0144005.  
 PR 16-JUL-1999; 99US-0144085.  
 PR 19-JUL-1999; 99US-0144086.  
 PR 19-JUL-1999; 99US-0144325.  
 PR 19-JUL-1999; 99US-0144331.  
 PR 19-JUL-1999; 99US-0144332.  
 PR 19-JUL-1999; 99US-0144333.  
 PR 19-JUL-1999; 99US-0144334.  
 PR 20-JUL-1999; 99US-0144335.  
 PR 20-JUL-1999; 99US-0144352.  
 PR 20-JUL-1999; 99US-0144632.  
 PR 20-JUL-1999; 99US-0144884.  
 PR 21-JUL-1999; 99US-0144814.  
 PR 21-JUL-1999; 99US-0145086.  
 PR 21-JUL-1999; 99US-0145088.  
 PR 22-JUL-1999; 99US-0145085.  
 PR 22-JUL-1999; 99US-0145087.  
 PR 22-JUL-1999; 99US-0145089.  
 PR 22-JUL-1999; 99US-0145192.  
 PR 23-JUL-1999; 99US-0145145.  
 PR 23-JUL-1999; 99US-0145218.  
 PR 23-JUL-1999; 99US-0145224.  
 PR 26-JUL-1999; 99US-0145276.  
 PR 27-JUL-1999; 99US-0145913.  
 PR 27-JUL-1999; 99US-0145918.  
 PR 28-JUL-1999; 99US-0145919.  
 PR 02-AUG-1999; 99US-0145951.  
 PR 02-AUG-1999; 99US-0146386.  
 PR 02-AUG-1999; 99US-0146388.  
 PR 03-AUG-1999; 99US-0146389.  
 PR 04-AUG-1999; 99US-0147204.  
 PR 05-AUG-1999; 99US-0147199.  
 PR 05-AUG-1999; 99US-0147260.  
 PR 06-AUG-1999; 99US-0147303.  
 PR 06-AUG-1999; 99US-0147416.  
 PR 09-AUG-1999; 99US-0147493.  
 PR 10-AUG-1999; 99US-0147935.  
 PR 11-AUG-1999; 99US-0148319.  
 PR 12-AUG-1999; 99US-0148341.  
 PR 13-AUG-1999; 99US-0148565.  
 PR 13-AUG-1999; 99US-0148684.  
 PR 17-AUG-1999; 99US-0149368.  
 PR 18-AUG-1999; 99US-0149426.  
 PR 20-AUG-1999; 99US-0149722.  
 PR 20-AUG-1999; 99US-0149723.  
 PR 20-AUG-1999; 99US-0149929.  
 PR 23-AUG-1999; 99US-0149930.  
 PR 25-AUG-1999; 99US-0150566.  
 PR 26-AUG-1999; 99US-0150884.  
 PR 27-AUG-1999; 99US-0151065.  
 PR 27-AUG-1999; 99US-0151066.  
 PR 30-AUG-1999; 99US-0151303.

Alignment Scores:  
 Pred. No.: 1.41e-155  
 Score: 1542.00  
 Best Local Similarity: 79.29%  
 Query Match: 67.93%  
 DB: 21

Length: 1703  
 Matches: 316  
 Conservative: 40  
 Mismatches: 47  
 Indels: 46  
 Gaps: 8

US-09-847-081B-2 (1-440) x AAC35120 (1-1703)  
 Qy 1 MetSerMetSerValAlaLeuLeuTrpValAla-----SerProThrSerGluValSerArg  
 Db 290 ATGTCTTCCTGAGCTGTATGGTTGCCTACTCTCTAAATCAGACCCAAATG 349  
 Qy 19 AsnGlyThrGlyLeuLeuAspSerValArgGluGlyAsnArgValPheValSerArg  
 Db 350 AACATTCCTGGTTGGTA-----AGGTCTAGAATCTCTAGA 388  
 Qy 39 PheLeuAlaArgAspArgAsnLeuMetTrpAsnGlyArgIleLysLysGlyGlyArgGln 58  
 Db 389 CTTGTCCTCCCTGTCGAAT-----CNG 412  
 Qy 59 ArgTrpAsnPheGlySerIleAlaAspProArgTyrSerCysLeuLeuGlySerArg  
 Db 413 AGCTAAACAAGGTAAGAAGACAGATAACCAACTGGAT-----

Qy	79	ThrGlutLySerThrPhe	-----	SerValGlnSer	89		Qy	427	LeuValProProAsnArgThrSerSer	435
Db	455	-----	-TCCTCTTGTGATGAAACCGAAGTAGAGAATAATGGTGTGCTTC	502			Db	1523	GTTACTA-----AGACTTCAGT	1540
Qy	90	serleuvalaserproAlaGlyGluMetThrValSerSerGluLysValTyroSp	109				RESULT 15			
Db	503	AGCTTAGTAGCAAGTCCCTCTGAGAGATAGCTCTCATCTGAGAAAGTTCAAT	562				AAV16948			
Qy	110	ValValLeuLysGlnAlaAlaLeuValValLysArgGlnLeuArgSerThrAsp	--AspLeu	128			ID	AAV16948	standard; cDNA to mRNA;	2085 BP.
Db	563	GTGGTGAAACAGCTGGTAAACACAGCTAACGTAAGTCCTCTATGATCT	622				XX			
Qy	129	GluValLys-----ProAspIleValIleProGlyAsnLeuGlyLeuLeuSerGluAla	146				DE		Nucleic acid encoding phytene synthase 1.	
Db	623	GATGTGAAAACCACAAAGATCTGTTCTCTGGGAGTTGAGTTGTTGGTGAAGCT	682				XX		Phytene synthase; breeding; variable flower colour; ds.	
Qy	147	TyrAspPheCysGlyGluValCysAlaGlyTrAlaLysThrPheTyLeuGlyThrLys	166				XX		Gentiana.lutea.	
Db	683	TATGATCGATGCGGTGAAGTTGCGCTGAATITGCTAAGACGTTTATCTGGAACTT	742				OS			
Qy	167	LeuMetThrProGluArgArgAlaIleThrPheAlaIleTyraIrrPheCysArgArgThr	186				Key		Location/Qualifiers	
Db	743	CTPATGACACCCAAAGCGAAAGGCCATTGGCPATCTACGTTGGTGTGAAAGACT	802				CDS	586..1866		
Qy	187	AspGluIleUvaIleAspGlyPheProAlaSerHisIleThrProGlnAlaLeuAspPhe	206				FT		/tag= a	
Db	803	GATGAACTTGTTGATGGCCCAAATGCTCACATACTCCATGGCTTATGATGG	862				XX			
Qy	207	GlutThrArgLeuGluAspIlePheSerGlyIaYgProPheAspMetLeuAspAlaLeu	226				PN			
Db	863	GAAGCAAGTTAGAAAGTCATCTTCGCGNNGCTCGATGCTGTAAGCTGCTCTC	922				PR	17-SEP-1996;	96JP-0245107.	
Qy	227	SerAspThrValSerArgPheProValAspIleGlnProPheArgAspMetIleGluGly	246				XX	17-SEP-1996;	96JP-0245107.	
Db	923	GCTGATACAGTCCTAGATACCTCTGTTACGCAATTAGCAGATTCGAGCATGTCAGGA	982				PA	(IWAT-) IWATE KEN.		
Qy	247	MetArgMetAspIlePheAspIlePheSerArgTrpLysThrPheAspGluIleUvaIleTyrcys	266				XX			
Db	983	ATGAAATGACTGAAATCGAGATACCAAACTCGATGATCTATACCTTTACTGC	1042				DR			
Qy	267	TytyrValAlaGlyThrValGlyIleMetSerValProValMetGlyIleAlaProGlu	286				DR	1998-264857/24.		
Db	1043	TACTACGTCGCTGAAACCGTCGATGACCGTTCCGGTTATGGGAATCTCTAAAG	1102				XX			
Qy	287	SerLysAlaThrThrGluSerValTyAsnAlaAlaLeuAlaLeuGlyLeuAlaAsnGln	306				PS			
Db	1103	TCGAAAGCAACACCGAAAGGTGTTACAACTGGCTGGCCCTTGTTAGCCAAATCAG	1162				PS			
Qy	307	LeuThrAsnIleLeuArgAspIleArgIleGlyGluAspAlaArgGlyArgValItyLeuPro	326				PS			
Db	1163	CTTACTAACTACTCAGAGAAACTCTCATGAAATGCGCTAAAGCGCAAGAATGCTCTCGACGAA	1342				XX			
Qy	327	GlnAspGluIleAlaGlnAlaGlyLeuUserAspGluAspIlePheAlaGlyArgValIthr	346				Qy	2.89e-154	Length:	
Db	1223	CAGGATGATTGGCTCAGCTGCTTCAGTGAACGAAAGTAACATTCGCGGAAAGTAAC	1282				Db	1551.00	Matches:	
Qy	347	AspIystPArgasnPheMetLysLysGlnIleGlnArgIalArgLyspheAspGlu	366				Qy	1	MetSerMetSerValAlaLeuLeuIleIleValSerProThrSerGluValSerAsnGly	20
Db	1283	GATAATGGAGAAACTCTCATGAAATGCGCTAAAGCGCAAGAATGCTCTCGACGAA	1342				Db	580	GTTAACATGTCATTGTTACGCTATGCTGTTGCTGAGTTGAGTTGAGTCGC	639
Qy	367	SerGluLysGlyIvalThrGluLeuAspSerAlaSerArgTrpValLeuThrAlaLeu	386				Qy	21	ThrGlyIleLeuAspSerValArgGluMetIlePheAspGluIleArgIleLysGlyGlyArgGlnArgTrp	40
Db	1343	GCIGAGAAAGGGTCACTGGAGCTAGTGGCTAGCATGGCTGATGGCTCTATG	1402				Db	640	AATGTTCTTGAGCCAAATTGAGAAAGT	675
Qy	387	LeuLeuTyArgLysIleLeuAspGluIleGluAlaAsnAspTyRhsAsnPheThrArg	406				Qy	41	AlaArgAspArgAsnLeuMetIlePheAspGluIleArgIleLysGlyGlyArgGlnArgTrp	60
Db	1403	CTATTGACAGGAAATFACTGGAGATGAGTGAAGCTGATGTTACACATTTACTAG	1462				Db	676	TTTCGATGATAGCTGTTGCTCCATTGAGTACGATGAGTACGATGACCAAGGGT	735
Qy	407	ArgAlaTyValSerLysProLysLysLeuLeuThrLeuProLeAlaLysSer	426				Qy	61	AsnPheGlySerIleLeuAlaAspProArgTyrsSerCysLeuGlyGlySerArgThrGlu	80
Db	1463	AGACCTTATGGGGAAAGTCAGAAATTGGCTTGTGCTTATGGCTTATGAGACTCTG	1522				Db	736	AGTACACGTTATGGGTTGGAGTCTGTTGAGACTCTG	795

Search completed: April 5, 2003, 03:09:15  
 Job time : 306 secs

Qy	Amino Acid Sequence	Db	Amino Acid Sequence
81	--LysglySerThrPhaser-VaGlnSerLeuValAlaSerProAlaGlyGluMe	796	ACCCGGAAAGAGATTATCGGTATCCTCATATTTAGCTAACCCGGAGGAAT
Qy	99 tThrValSerGlnIysLysValTyrAspValValLeuIysGlnAlaAlaLeuVally	856	GACATGACATGAGAAAAGTTATGATTCGTTAARGCAACGAGCTTGATAA
Qy	119 sArgGlnLeuValAspLeuGluValLysProAspIleValProGlyAs	915	TAGACACTTGAGCTPAGAGAAAATTTGGAGTGAACCGGACATTTTCAGGAAA
Qy	139 nIleGlyLeuLeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGluTyraLys	975	CCGAAAGCTGTGAATTAAGCTTATGTCGGTGCAGAAAGTATGCTGATATGCCAA
Qy	159 sThrPhetyLeuGlyThrLysLeuMetThrProGluArgArgAlaIleTerPala--	1034	GRCATCTACTGGGAACCCAGCTCATGACACCGGAGGGTTAGCTAATCTGGCCGA
Qy	179 -IleTerValTrpCysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisI	1094	AAATCCACCCGGTTAGATCGGTGAGGACAGATGAGCTGTTGATGGCCPNAACGCTCACCAT
Qy	1095 TRATAATGTAATGCGTGTGAGGACAGATGAGCTGTTGATGGCCPNAACGCTCACCAT	1154	1154
Qy	198 ethrProGlnAlaLeuAspArgTrpGluThrArgLeuGluAspIlePheSerGlyArgPr	1155	AAATCCACCCGGTTAGATCGGTGAGGACAGATGAGCTGTTGATGGCCPNAACGCTCACCAT
Qy	218 oPheAspMetLeuAspAlaLeuSerAspThrValSerArgPheProValAspIleG	1214	1214
Qy	225 TCTGGATATGCTGATCTGCTTATGTGATCATACCAGTATCTGGACACCCA	1274	1274
Qy	238 nProPheArgAspMetIleGluGlyMetArgMetAspIleTrpLyserArgTyrlYstH	1275	GCCTTAAGTAGATGATGAGGAATGGATGGACTGAGAAATCGAGATAACGAA
Qy	1275 GCCTTAAGTAGATGATGAGGAATGGATGGACTGAGAAATCGAGATAACGAA	1334	1334
Qy	258 rPheAspGluLeuTyreLeuTyrcystyTyryValAlaGlyThrValGlyLeuMetSerVa	1335	TTTCGATGAGCGCTGATATTCTACTGCFATTATGTCGGCCACAGTGGCTGATGAGTGT
Qy	1335 TTTCGATGAGCGCTGATATTCTACTGCFATTATGTCGGCCACAGTGGCTGATGAGTGT	1394	1394
Qy	278 lProValMetGlyIleAlaProGluSerLysAlaThrThrGluSerValTyraAlaAl	1395	ACCAGTATGGCATTGACCTGAATTAAAGCAACACAGAAAGTGTGATGGAGC
Qy	1395 ACCAGTATGGCATTGACCTGAATTAAAGCAACACAGAAAGTGTGATGGAGC	1454	1454
Qy	298 aLeuAlaLeuGlyLeuAlaAsnGlnIleThrAsnIleLeuIargAspValGlyGluAspAl	1455	TTATCATGGGATGCCGAACCGTGAACATCTAACGGGAACTTGGAGCTGAGAAACTG
Qy	1455 TTATCATGGGATGCCGAACCGTGAACATCTAACGGGAACTTGGAGCTGAGAAACTG	1514	1514
Qy	318 ArgArgGlyArgValTerLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspG	1515	AAGAAGGGAGACTGPAACCTGAAAGTTACAGACAATTCAGAAATTTATGAGAAAGCAATCAA
Qy	1515 AAGAAGGGAGACTGPAACCTGAAAGTTACAGACAATTCAGAAATTTATGAGAAAGCAATCAA	1574	1574
Qy	338 uAspIlePheAlaGlyArgValThrAspIleTrpArgAsnPheMetIlysGlnIleG	1634	1634
Qy	338 uAspIlePheAlaGlyArgValThrAspIleTrpArgAsnPheMetIlysGlnIleG	1635	AAGGGCTAGAAAATTCTATGATGATGAGCAAAAGGTCCCGAATCTACGCTCCGAG
Qy	1635 AAGGGCTAGAAAATTCTATGATGAGCAAAAGGTCCCGAATCTACGCTCCGAG	1694	1694
Qy	378 rArgTrpProValLeuIleLeuIleLeuIleLeuAspGluIleGluAl	1695	CGATATCCCTGTGGCAGGGTTTATGAAAAATATTGATGAGATAAGGC
Qy	378 rArgTrpProValLeuIleLeuIleLeuIleLeuAspGluIleGluAl	1754	1754
Qy	398 aAsnAspTyrAsnAspPheThrArgAlaTyrValSerIysProIysLysLeuLeuI	1755	AAATGACTACACRAATTGCCAGAGGGCTATGTAACSGGGSRAGAAGCTATAGC
Qy	398 aAsnAspTyrAsnAspPheThrArgAlaTyrValSerIysProIysLysLeuLeuI	1814	1814
Qy	418 rLeuProIleAlaTyrAlaTyrSerIeu	1815	TTATGCTCTGAACTGATGCTCCGAGTCCTGCTTC
Qy	418 rLeuProIleAlaTyrAlaTyrSerIeu	1847	1847